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Variations in Meristic and Morphometric Characters among Populations of Herring *Clupea pallasii* in the Far Eastern Waters*1

Yasuji Kanno*2

(Received July 16, 1988)

In order to investigate morphological variations in the ten herring populations in the Far Eastern waters, five meristic and five morphometric characters on body length were examined by employing statistical analysis.

No significant difference was recognized between sexes in all characters except for a BW/BL relation, and significant differences among ten populations were recognized in nine characters except pelvic fin rays. The number of pairs of populations showing significant differences in five characters or more was 31 (69 percent) of all combinations suggesting the diversity of the stocks.

Four groups were distinguished by cluster analysis using Mahalanobis's generalized distances with nine characters and, further, the coefficients of differences on the head length-body length relation showed such large values as to suggest status of subspecies between the groups of the highest distances.

The author in the preceding report[1)] reported on the variations in age composition and growth as well as the existence of ecological polymorphism with respect to ten herring populations distributed in Far Eastern waters. To study the fundamental questions of herring ecology such as further clarifying the morphological variations among these populations and discovering the connection with the quantitative characteristics of the populations as well as examining the ramification process of the ecology of the populations, is thought to be valuable in connection with long-term forecasts of the herring resource, conservation of the resource and utilization as a seed resource, etc. In this report, by statistically analyzing the morphological characters such as the

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meristic characters and morphometric characters, the relationship among populations looked at from a morphological perspective has been reported on.

Materials and method

The materials used in the study were samples from the ten regional populations reported in the preceding report.[1)] The measurements as a rule were done on 80 or more individuals per sample. In terms of measurement, after determining the sex, the calculation of the five meristic characters of number of pelvic fin rays (PF), number of anal fin rays (AF), number of vertebrae (VN), and number of upper gill rakers (UGR) and number of lower gill rakers (LGR) on the first branchial arch on the right side, and the measurement of five body part lengths were carried out. For the number of anal fin rays the rays clearly separated at the base were counted, for the gill rakers only those where xiphoid or foliated gill rakers were formed were counted, and for the vertebrae the total number including the caudal cylindrical bones, without distinguishing between ventral vertebrae and caudal vertebrae, was counted.

The measurement of the body part lengths was done with respect to the standard body length BL and the preanal length PAL, head length HL, predorsal length PD, prepelvic length PP shown in Fig. 1, and as a weight character the gonadectomized body weight BW was weighed. The relationship between these

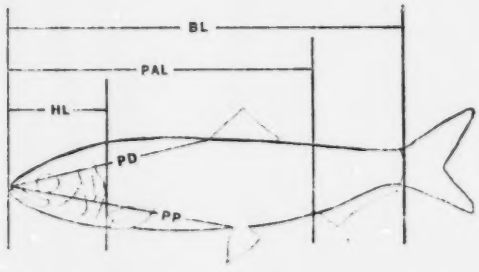

Fig. 1. Measurement of herring body parts for morphometrical analysis, **BL**: body length, PAL: preanal length, HL: head length, PD: predorsal length, PP: prepelvic length.

characters was analyzed using the allometry equation $\log Y = \log b + k \cdot \log X$ (432) taking the standard body length as the base length X and the body part lengths and BW as Y.[2] Here, $\log b$ is the slice and k is a morphometric coefficient. With respect to these morphometric characters, the handling of the distance characters and weight character was lumped together, and a style of expression was adopted such that a head length - body length relationship would be expressed as HL/BL.

Results

Meristic characters. Before analyzing the variations among populations, the difference between female and male in character variation was investigated by a t-test and the difference between age groups by analysis of variance. The occurrence of significant differences in the tests between sexes and between ages was extremely rare, and any variation due to these two factors was judged to be attributable to error components based on chance fluctuations, so that the analysis of variations among populations was proceeded with using samples in which the sexes and age groups were lumped together.

In order to investigate the difference in character variation among populations, a test on the homogeneity of the sample means was done by analysis of variance, as a result of which significant differences were discerned in four characters (AF, VN, UGR, LGR) excluding PF (Table 1). The characteristics of the variation in the four characters indicating significant differences (Table 2) and the t-test results between pairs of populations (Table 3) are as follows.

1 Number of anal fin rays. Varying in the range of 13 - 19, the variation range is 6. The modes are found in 15 - 16. The mode in 15 is in Obuchi Marsh and DeKastri, while the other eight populations have a mode in 16. The maximum population mean is 16.4 (Notoro Lake) and the minimum is 15.5 (Obuchi Marsh), their difference being approximately 0.9. In the t-test results, among the 45

combinations significant differences were seen in 21 combinations (47%).

2 Number of vertebrae. Varying in the range of 52 - 57, the variation range is 5. The mode for all samples was in 54. Looking at the skew from the mode, the samples from Furen Lake, Notoro Lake and DeKastri comprise a high ratio of those 53 and under, while the others have a high ratio of those 55 and over. The minimum population mean is 53.7 (Notoro Lake, DeKastri) and the maximum is 54.4 - 54.5 (Obuchi Marsh, Atsuta, Karaginski), their difference being approximately 0.8. In the t-test results, among the 45 combinations significant differences were seen in 28 (62%). (433)

Table 1. Variance analysis in the means of ten populations for five numerical characters

Numerical character	Between samples		Between individuals		F ratio
	Variance	*df*	Variance	*df*	
Pelvic fin rays	0.134	9	0.078	786	1.7*
Anal fin rays	6.678	9	0.664	789	10.1*
Vertebrae	6.253	9	0.441	774	14.2*
Upper gill rakers	7.656	9	0.812	750	9.4*
Lower gill rakers	38.483	9	2.667	758	14.4*

* Significant at 1% level.

Table 2. Frequency distribution for four numerical characters of samples caught from ten localities

Locality	Anal fin rays							Vertebrae					
	13	14	15	16	17	18	19	52	53	54	55	56	57
Obuchi	0	6	37	24	13	0	0	0	4	44	27	4	1
Yūdō	0	5	23	34	16	1	0	0	9	50	20	0	0
Fūren	0	1	23	46	11	0	0	0	19	44	16	2	0
Atsuta	0	2	18	44	16	0	0	0	3	44	27	4	0
Notoro	0	2	7	36	27	7	1	3	26	41	10	0	0
Saroma	0	2	9	40	30	5	0	0	6	42	28	2	1
DeKastri	1	3	29	25	8	1	0	1	19	41	5	0	0
Okhotsk	0	2	24	40	11	3	0	0	2	48	28	2	0
Karaginski	0	5	26	36	13	0	0	0	2	41	33	5	0
Gizhiga	0	3	32	45	16	0	0	0	7	53	30	0	0

Locality	Upper gill rakers						Lower gill rakers									
	18	19	20	21	22	23	41	42	43	44	45	46	47	48	49	50
Obuchi	4	22	33	18	3	0	1	3	13	19	16	18	9	1	0	0
Yūdō	2	9	35	31	3	0	1	3	9	18	15	17	12	5	0	0
Fūren	0	6	30	33	10	2	0	1	2	19	21	21	12	4	1	0
Atsuta	0	8	32	27	12	1	0	1	4	12	23	23	10	3	2	1
Notoro	0	7	30	28	11	3	0	0	1	10	19	21	17	9	1	2
Saroma	0	4	22	40	13	1	0	0	0	8	23	24	13	15	5	0
DeKastri	0	6	18	36	4	2	0	0	2	13	15	17	15	2	1	1
Okhotsk	0	2	28	27	16	2	0	0	4	7	15	22	16	5	3	3
Karaginski	0	6	15	29	17	5	0	1	4	6	9	16	18	10	6	2
Gizhiga	0	2	25	29	19	1	0	0	0	1	8	12	21	21	12	1

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Table 3. Characters with significant differences at the 5% level for each pair among ten populations. The characters are four numerical characters (+1: AF, +2: VN, +3: UGR, +4: LGR), log-log length-weight regression (•1: BW/BL) and four morphometric characters (•2: PAL/BL, •3: HL/BL, •4: PD/BL, •5: PP/BL). Notations are in text

Locality	Obuchi	Yūdō	Furen	Atsuta	Notoro	Saroma	DeKastri	Okhotsk	Karaginski	Gizhiga
Obuchi										
Yūdō										
Fūren										
Atsuta										
Notoro										
Saroma										
DeKastri										
Okhotsk										
Karaginskii										
Gizhiga										

3 Number of upper gill rakers. Varying in the range of 18-23, the variation range is 5. The modes were found in 20 - 21. The mode in 20 is seen in the five samples from Obuchi Marsh, Yudo Marsh, Atsuta, Notoro Lake and Okhotsk, while the other samples have a mode in 21. The minimum population mean is 19.9 (Obuchi Marsh) and the maximum is 21 (Karaginski), their difference being approximately 1.1. In the t-test results, among the 45 combinations significant differences were seen in 22 (49%).

4 Number of lower gill rakers. Varying in the range of 41 - 50, this is the most variable character among the compared characters. The modes extend over 44 - 48. The mode in 44 is in the two samples from Obuchi Marsh and Yudo Marsh, the modes in 45 - 46 are in the two samples from Furen Lake and Atsuta, the mode in 46 is in the four samples from Notoro Lake, Saroma Lake, DeKastri and Okhotsk, and the highest modes in 47 - 48 are in the two samples from Karaginski and Gizhiga Bay. In general the population mean of the populations around Japan is low, and the further north a population is located, the higher it is. In the t-test results, among the 45 combinations significant differences were seen in 31 (69%).

Morphometric characters. The relationships corresponding to the allometry equation when the standard body length (BL) was taken as the base length X and the body part lengths (preanal length PAL, head length HL, predorsal length PD, prepelvic length PP) and gonadectomized body weight (BW) were taken as Y, were first of all investigated. As a result, in the three characters of HL/BL, PD/BL, PP/BL, there was a refraction point at body length 168 mm, before and after which a linear relationship with a different slope was indicated. Given this result, in the analyses below, the allometry relations formed by the body length groups above 168 mm to which the majority of the samples belong, shall be compared.

Upon examining the difference between the sexes with regard to the slope (gradient) of the morphometric lines and adjusted means (heights) by analysis of covariance,[3] significant differences were seen in the adjusted means of six of the ten populations in the case of BW/BL, in the slope of two populations and adjusted mean of one population in the case of PAL/BL, and in the adjusted mean of one population in the case of PP/BL. With HL/BL and PD/BL, no significant differences could be discerned in either slope or adjusted mean.

Next, in order to investigate the difference among populations, the homogeneity of the morphometric lines among populations with respect to five morphometric characters (BW/BL, PAL/BL, HL/BL, PD/BL, PP/BL) was examined by analysis of covariance[3] for the three cases of female, male and both sexes together (Table 4). Note that samples indicating a low correlation below 0.7 were not included in the calculations. The results of this were that no significant differences were discerned in the case of slope in any characters for either female or male, but in the case of adjusted mean significant differences were indicated in all characters.

From the foregoing analyses, it was clear that a difference exists (435)
between the adjusted means for female and male in the case of BW/BL and that

Table 4 Results of covariance analysis regarding homogeneity in slopes and adjusted means among ten samples for log-log length-weight regression and four log-log relationships between body part lengths and body length. Notations are in text

Relationship	Female		Male		Whole	
	Slope $F_0(df)$	Adjusted mean $F_0(df)$	Slope $F_0(df)$	Adjusted mean $F_0(df)$	Slope $F_0(df)$	Adjusted mean $F_0(df)$
BW/BL	1.282 (8,336)	27.014*1 (8,344)	1.792 (9,327)	30.884*1 (9,336)	2.026*2 (8,467)	59.656*1 (8,659)
PAL/BL	0.685 (9,391)	3.621*1 (9,400)	1.907 (9,328)	3.745*1 (9,337)	1.352 (9,771)	7.166*1 (9,780)
HL/BL	1.620 (7,294)	77.002*1 (7,301)	0.738 (8,287)	85.873*1 (8,295)	0.890 (8,673)	232.992*1 (8,681)
PD/BL	0.666 (8,339)	8.825*1 (8,347)	0.706 (9,326)	4.501*1 (9,335)	0.824 (9,770)	13.921*1 (9,779)
PP/BL	1.832 (8,339)	16.417*1 (8,347)	1.285 (9,327)	8.573*1 (9,336)	2.683*1 (9,771)	25.163*1 (9,780)

*1 Significant at 1% level.
*2 Significant at 5% level.

Table 5. Two constants k and $\log b$ of the equation $Y=bX^k$ in males and females for log-log length-weight regression

Locality	Female				Male				Whole			
	k	$\log b$	r	Adjusted mean	k	$\log b$	r	Adjusted mean	k	$\log b$	r	Adjusted mean
Obuchi	2.819	−4.441	0.857	2.222	2.557	−3.812	0.911	2.199	2.704	−4.164	0.876	2.111
Yūdō	3.325	−5.578	0.983	2.294	3.198	−5.285	0.978	2.258	3.286	−5.490	0.981	2.278
Fūren	3.075	−5.000	0.827	2.278	2.728	−4.207	0.870	2.237	2.980	−4.786	0.848	2.260
Atsuta	2.759	−4.258	0.933	2.273	2.392	−3.420	0.881	2.230	2.816	−4.398	0.921	2.257
Notoro	2.853	−4.520	0.905	2.247	3.190	−5.324	0.958	2.188	3.191	−5.316	0.935	2.217
Saroma	3.213	−5.356	0.938	2.242	3.194	−5.329	0.952	2.195	3.226	−5.394	0.944	2.220
DeKastri	3.150	−5.211	0.949	2.244	3.143	−5.182	0.967	2.231	3.145	−5.193	0.959	2.238
Okhotsk	3.240	−5.432	0.871	2.238	3.461	−5.992	0.882	2.187	3.248	−5.467	0.854	2.211
Karaginski	3.610	−6.357	0.763	2.207	3.344	−5.752	0.780	2.148	3.233	−5.466	0.717	2.179
Gizhiga	2.774	−4.326	0.636	2.239	2.915	−4.675	0.711	2.197	2.836	−4.479	0.666	2.220

Table 6. Two constants k and $\log b$ of the equation $Y = bX^k$ for four log-log relationships between body part lengths and body length

Locality	PAL/BL				HL/BL				PD/BL				PP/BL			
	k*1	$\log b$	r	Adjusted mean	k*2	$\log b$	r	Adjusted mean	k*1	$\log b$	r	Adjusted mean	k*1	$\log b$	r	Adjusted mean
Obuchi	1.031	−0.200	0.985	2.237	0.840	−0.288	0.950	1.699	0.990	−0.279	0.959	2.061	1.098	−0.496	0.965	2.101
Yūdō	1.036	−0.217	0.989	2.233	0.820*3	−0.239	0.968	1.698	0.983	−0.266	0.981	2.059	1.056	−0.390	0.975	2.107
Fūren	0.993	−0.112	0.995	2.235	0.796*3	−0.180	0.896	1.702	0.999	−0.299	0.896	2.062	0.899	−0.017	0.872	2.111
Atsuta	0.940	0.013	0.966	2.234	0.778*3	−0.128	0.900	1.711	0.927	−0.132	0.915	2.060	0.899	−0.008	0.920	2.118
Notoro	1.015	−0.163	0.978	2.237	0.793	−0.171	0.888	1.704	0.953	−0.189	0.945	2.067	0.968	−0.183	0.956	2.107
Saroma	1.021	−0.175	0.981	2.239	0.779*3	−0.149	0.887	1.693	1.017	−0.340	0.964	2.062	0.962	−0.171	0.951	2.106
DeKastri	0.994	−0.111	0.966	2.238	0.819	−0.222	0.921	1.715	0.947	−0.177	0.925	2.061	0.943	−0.109	0.925	2.117
Okhotsk	1.040	−0.221	0.950	2.238	0.940	−0.489	0.859	1.738	1.016	−0.336	0.903	2.068	1.079	−0.438	0.858	2.115
Karaginski	1.116	−0.164	0.927	2.237	0.803	−0.147	0.790	1.751	0.889	−0.027	0.806	2.071	1.128	−0.556	0.808	2.116
Gizhiga	0.925	0.052	0.872	2.237	0.718*3	0.028	0.568	1.725	0.838	−0.031	0.708	2.068	1.074	−0.424	0.762	2.116

*1 isauxesis.
*2 isauxesis or bradyauxesis.
*3 significant at 5% level for $H_0: k = 1$.

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a difference which exceeds the sampling error level exists in the adjusted means of the five morphometric characters among populations. The characteristics among populations of the morphometric lines for each character can be shown as follows (Table 5, Table 6).

1 BW/BL. The value of slope k varies from 3.61 (Karaginski ♀) to 2.39 (Atsuta ♂), and in neither female nor male can a significant difference among populations be discerned. In the adjusted mean, however, significant differences can be discerned. The adjusted mean is highest for both sexes at Yudo Marsh (♀: 2.294, ♂: 2.258) and lowest at Karaginski (♀: 2.207, ♂: 2.148), with the rank order of the populations in the sexually differentiated cases generally corresponding.

2 PAL/BL. The value of k varies from 0.93 (Gizhiga Bay) to 1.12 (Karaginski), all indicating isauxesis. The adjusted mean varied between 2.233 (Yudo Marsh) and 2.239 (Saroma Lake).

3 HL/BL. The correlation coefficient for Gizhiga Bay was a low 0.57, but elsewhere a high value of 0.79 or above is shown. The value of k varies from 0.72 (Gizhiga Bay) to

0.94 (Okhotsk), indicating bradyauxesis. The adjusted mean varies in range from 1.693 (Saroma Lake) to 1.751 (Karaginski), with a high value being indicated in three populations in northern waters.

4 PD/BL. The value of k varies from 0.89 (Karaginski, Gizhiga Bay) to 1.02 (Saroma Lake, Okhotsk), indicating isauxesis. The adjusted mean varies in range from 2.059 (Yudo Marsh) to 2.671 (Karaginski), it being high generally in the populations in northern waters.

5 PP/BL. The value of k varies from 0.90 (Furen Lake, Atsuta) to 1.13 (Karaginski), indicating isauxesis. The adjusted mean varies in range from 2.101 (Obuchi Marsh) to 2.117 (DeKastri), with a high value being indicated in the four populations in northern waters and the population at Atsuta.

Summary of morphological variation among populations. Looking at the number of characters which indicate significant differences in the examination concerning means or adjusted means for the 45 combinations among the populations (Table 3), taking the meristic characters and morphometric characters together, at least two or more significant characters were discerned among all combinations. The number of combinations with a high degree of heterogeneity which indicate significant differences in five or more characters was 31, comprising 69% of all combinations. The populations with the most differences with other populations were Obuchi Marsh, Yudo Marsh, Atsuta and DeKastri, in which the number of combinations which indicate significant differences in five or more characters is eight or seven. Conversely, the population with the least differences with other populations was the Saroma Lake population, in which the combinations which indicate significant differences in five or more characters number four. Looking at it regionally, the three populations of Okhotsk, Karaginski and Gizhiga Bay in northern waters have a relatively small number of significant characters in the combinations among themselves, indicating 2 - 4 characters, whereas in the combinations of the six populations around Japan the number of

significant characters was 3 - 8, reflecting the existence of a variety of stages. The number of significant characters of the DeKastri population vis-a-vis both the six populations around Japan as well as the three populations in northern waters is fairly high at 4 - 7.

Morphological distance among populations. The heterogeneity among populations will enable the rendering of a tentative evaluation by the number of significant characters among each other, but in the case where there are characters with a strong connection in the tendency of variation like UGR and LGR, there are instances where results occur in which the overall evaluation differs greatly depending on the type of characters adopted. This kind of drawback associated with multi-character analysis can be avoided by using Mahalanobis's generalized distance D^2. This D^2, under conditions where each character is equally dispersed and normally distributed in two populations i, j, is calculated by

$$D^2=(X_i-X_j)'\sum^{-1}(X_i-X_j)$$

while D^2 and the probability of error P(e) correspond to a unit normal distribution function as[4)]

$$P(e)=\int_{\frac{1}{2}\sqrt{D_{ij}^2}}^{\infty}\frac{1}{\sqrt{2\pi}}\exp\left(-\frac{z^2}{2}\right)dz$$

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so that it has the added advantage of being able to evaluate the heterogeneity among populations as a probability. Using the nine characters in which the variation among populations as compared to the variation among individuals was found to be significant, Mahalanobis's D^2 and the percent overlap[5)] among populations calculated as twice the error rate are shown in Table 7. In the calculation, for the meristic characters the measured values were used intact, while for the morphometric characters the deviation between the predicted (437) regression lines having a common slope and passing through the aggregate mean point (mean coordinates of log X and log Y) and the measured values for each

individual has been used in the calculation.

Looking at Table 7, the combinations of populations in which Mahalanobis's distance is great and the percent overlap is under 5% come to 11 pairs (24%) out of 45 combinations, all of which are combinations between the three populations of Okhotsk, Gizhiga Bay and Karaginski and the seven populations excluding them. On the other hand, the combinations of populations which indicate a large percent overlap over 40% are the five pairs (11%) of Furen Lake - Yudo Marsh, Furen Lake - Atsuta, Notoro Lake - Saroma Lake, DeKastri - Atsuta and Furen Lake - DeKastri.

Table 7. The Mahalanobis's generalized distance (lower triangle) and the percent overlap (upper triangle) for each pair among ten populations calculated by employing nine morphological characters. Four groups are composed of samples merged by cluster analysis (see Fig. 2) using the Mahalanobis's generalized distance

Locality	1st group*				2nd group*			3rd group*		4th group*
	Yūdō	Atsuta	Fūren	De-Kastri	Obuchi	Notoro	Saroma	Okhotsk	Kara-ginski	Gizhiga
Yūdō		33.204	63.122	24.604	21.130	16.759	20.408	1.928	0.158	7.186
Atsuta	3.749		43.540	45.930	13.104	16.453	12.356	10.310	1.640	26.700
Fūren	0.914	2.430		41.222	26.700	29.372	29.834	4.236	0.437	14.429
DeKastri	5.428	2.190	2.667		19.705	24.604	15.272	17.069	3.001	40.090
Obuchi	6.269	9.082	4.937	6.625		28.462	35.238	3.156	0.410	8.363
Notoro	7.647	7.678	4.451	5.396	4.620		43.540	5.238	0.693	14.706
Saroma	6.494	9.455	4.358	8.154	3.442	2.451		1.685	0.158	7.345
Okhotsk	21.968	10.591	16.488	7.555	18.522	15.064	22.921		39.532	35.758
Karaginski	39.828	22.968	32.437	18.808	32.952	29.095	39.948	2.915		10.740
Gizhiga	13.004	4.901	8.545	2.851	11.931	8.361	12.884	3.353	10.419	

* Merged by cluster analysis.

Table 8. Coefficients of difference as to the BW/BL (upper triangle) and HL/BL (lower triangle) relationships for each pair among ten populations calculated by employing nine morphological characters. Four groups are composed of samples merged by cluster analysis (see Fig. 2) using the Mahalanobis's generalized distance

Locality	1st group*				2nd group*			3rd group*		4th group*
	Yūdō	Atsuta	Fūren	De-Kastri	Obuchi	Notoro	Saroma	Okhotsk	Kara-ginski	Gizhiga
Yūdō		0.374	0.278	0.770	0.966	0.993	0.842	1.028	1.452	0.912
Atsuta	0.716		0.058	0.384	0.686	0.674	0.551	0.728	1.178	0.603
Fūren	0.231	0.562		0.402	0.673	0.660	0.550	0.710	1.121	0.597
DeKastri	0.994	0.263	0.868		0.421	0.369	0.273	0.444	0.933	0.307
Obuchi	0.074	0.710	0.173	1.015		0.087	0.125	0.009	0.395	0.121
Notoro	0.301	0.326	0.129	0.561	0.261		0.050	0.083	0.529	0.040
Saroma	0.198	0.747	0.387	0.958	0.267	0.417		0.124	0.530	0.011
Okhotsk	2.051	1.435	2.050	1.238	2.159	1.558	1.791		0.429	0.119
Karaginski	2.942	2.293	3.037	2.103	3.140	2.314	2.462	0.667		0.548
Gizhiga	1.301	0.706	1.228	0.502	1.342	0.906	1.206	0.593	1.266	

* Merged by cluster analysis.

1. Coefficient of difference. In order to investigate the relationship among populations from a taxonomic aspect, with the same data used in Mahalanobis's D^2, Mayr's[6] coefficient of difference was calculated for each character. The coefficient of difference, with 1.28 (75% separation standard) as the critical point, is deemed to be a standard of difference of subspecies within a species.[6] Among the nine characters, in seven of the characters excluding BW/BL and HL/BL, no C.D. exceeding 1.0 in value was obtained in any of the combinations of populations, so that only the results of the two aforementioned characters are shown in Table 8.

Where a C.D. value above 1.0 was indicated for BW/BL was in four pairs (7%) among the 45 combinations of ten populations, all of which were combinations between the populations of Okhotsk and Karaginski and those around Japan (Yudo Marsh, Furen Lake, Atsuta). A value exceeding the critical value of 1.28 was discerned in only the one pair of Yudo Marsh - Karaginski. For HL/BL, the combinations with a C.D. value over 1.28 numbered 15 pairs (36%), 14 of which, excluding the one pair of DeKastri - Karaginski, were combinations between three populations in northern waters and the six populations around Japan.

2. Relationship among populations. In order to grasp the relative degree of relationship of populations in a simple form, cluster analysis was done using Mahalanobis's D^2 values. As a result, in terms of relationships which have a distance of 5 or more in D^2 value, the four groups shown in Fig. 2 were distinguished.

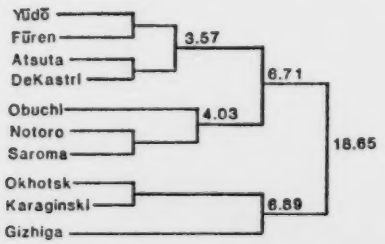

Fig. 2. Relationship among ten populations merged by cluster analysis using the Mahalanobis's generalized distance employing nine morphological characters.

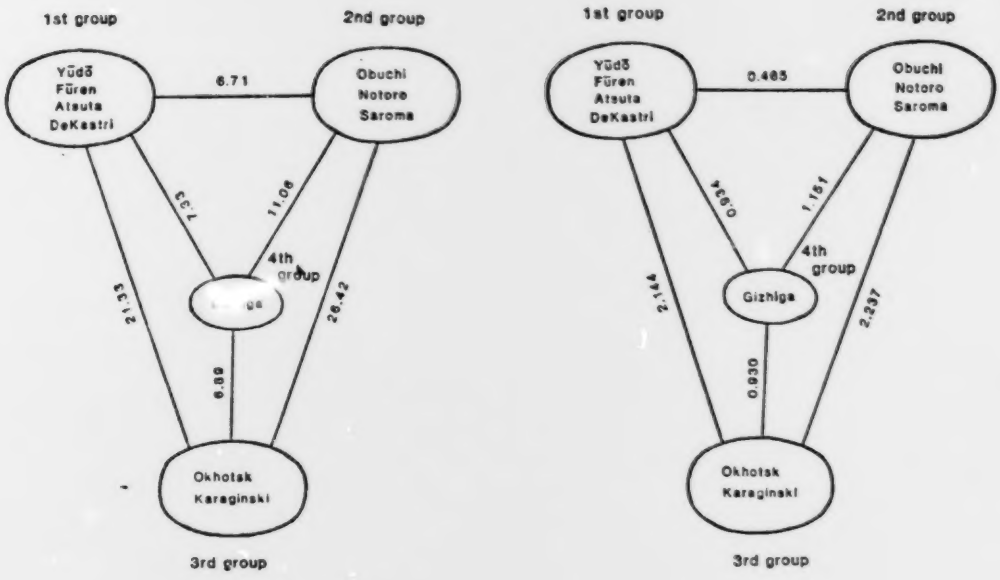

Fig. 3. Four groups of populations by cluster analysis using the Mahalanobis's generalized distance. Figures on solid lines between groups show the mean values of Mahalanobis's D^2(a) and the coefficients of differences of HL/BL(b).

Specifically, they were Group 1 consisting of the four populations of Yudo Marsh, Furen Lake, Atsuta, DeKastri, Group 2 consisting of the three populations of (438)
Obuchi Marsh, Notoro Lake, Saroma Lake, Group 3 consisting of the two populations of Okhotsk and Karaginski, and Group 4 consisting of the population of Gizhiga Bay. When the relationship among populations is shown by the means between the groups calculated from Mahalanobis's D^2 values and the coefficients of difference of HL/BL, Fig. 3 is obtained. The coefficients of difference show a high value exceeding 2.1 between Groups 1 and 2 and Group 3.

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Discussion

With regard to the classification of herring, there are a number of differing views. The widely accepted views of Lissner,[7] Krefft,[8] Einarsson,[9] and Parrish and Saville[10] claim that the Pacific herring and Atlantic herring are distinct species, and subdivide each into several further subspecies. By contrast, Shmidt,[11] Svetovidov,[12] and Marty[13] claim that the Atlantic

herring and Pacific herring are subspecies, and take the view of subdividing the fish groups below this as a race or form. In 1958, Blaxter[14] consolidated the taxonomic, physiological and genetic knowledge of recent years, and took the view of grouping the Atlantic herring into two sibling species and many subspecies included therein.

According to Parrish and Saville,[10] such differences in the views of researchers are mainly due to a lack of knowledge concerning the ramification of populations and the genetic basis thereof. This situation is the same with the Pacific herring as well, and while there are numerous studies of the population structure of herring distributed in Far Eastern waters by Svetovidov,[12] FUJITA and KOKUBO,[15] HANAMURA[16] and ISHIDA[17] et al., detailed inquiries concerning the taxonomic ranking of distinguished populations have virtually never been done. This kind of study will provide important information for considering various resource-oriented questions such as the process of group formation of populations or the connection to quantitative fluctuations, so that we would like to pursue it taking up mainly these points.

Rules of terminology. In Japan, fish groups which constitute units of resource fluctuation are called a lineal group or genealogical group. According to KUBO and YOSHIHARA,[18] pointing to fish groups distinguishable morphologically, ecologically, serologically or piscatologically at levels below species or below subspecies, it is claimed they more or less correspond to the infrasubspecific form in the Animal Designation Agreement[19] revised at the 13th International Animal Conference. In this way, the terminology genealogical group is a somewhat ambiguous term that contains equivocal taxonomic and ecological import, and is thought to correspond to race (geographical race), spawning group, tribe, stock, population, subpopulation, form (local form) and such. What are called spawning group, tribe, stock, population, subpopulation all refer to self-propagating groups, but have no taxonomic hierarchical meaning and are ecological groups.

The most elemental propagating group is called by the name spawning group or local population, but this is equivalent to the meaning of deme[20] in taxonomy. Contrary to this, race and form are taxonomic notions, race being below the rank of species, with some researchers (Einarsson[9]) saying it is synonymous with subspecies, but many researchers[21] in the ichthyological field have established the rank of geographical race below subspecies, claiming it refers to a self-propagating group of a genetically different level. Form is a rank below geographical race, and may be thought of as referring to a propagating group that differs only in phenotype in 1 - 2 characters.[7]

Population structure of herring. As a result of analyzing in detail the variation of nine characters with respect to ten populations distributed in Far Eastern waters, it was confirmed that there is a statistical difference in many of the characters between pairs of populations (Table 3). Furthermore, by means of cluster analysis using Mahalanobis's D^2 among populations, a population structure consisting of the four groups shown in Fig. 3 was made clear. The characteristics that can be seen in this figure are that, firstly, the relationships between Groups 3 consisting of Okhotsk and Karaginski and Groups 1 and 2 containing the six populations around Japan all have a value over 20 in Mahalanobis's D^2 and over 2.1 in the coefficient of difference, and reflect distances which correspond to subspecies according to Mayr's[6] standard. This can be thought to be related to differences in environment based on geographic distance, but like the populations of DeKastri and Gizhiga Bay, even though geographically distant there are those which are closely akin to the populations around Japan morphologically. The second characteristic is the fact that the populations around Japan can be separated into Group 1 consisting of the populations of Yudo Marsh, Furen Lake and Atsuta and Group 2 consisting of the populations of Obuchi Marsh, Notoro Lake and Saroma Lake. The distance between these groups is not that great considering the values of Mahalanobis's D^2 (6.712) and

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the coefficient of difference (0.459). Group 1 includes both populations that reflect an ecology of lentic spawning like Yudo Marsh and Furen Lake and the populations of Atsuta and DeKastri which spawn on the coast, while Group 2 includes populations located in the northern side of Japanese waters like Notoro Lake and Saroma Lake and the population of Obuchi Marsh located more southerly, so that they are not made up only of populations which are akin geographically and ecologically.

Summarizing the foregoing, the lineal groups (regional populations) of herring which are distributed in Far Eastern waters but differ in spawning grounds can be combined into four clusters differing morphologically in varying degrees, the maximum difference of which can be said to reach the difference of subspecies more or less. This fact can be supported from the growth and ecological differences reported in the preceding report[1)] as well. While these relationships between the clusterized populations are thought to be related to the population formation history of each,[12)] the details of this will be left as a subject of future research. Also, the ground for judging them as subspecies in the discussion in the preceding paragraph is based on the value of the coefficient of difference of HL/BL, but considering the fact that this character is a character with a strong correlation to the latitude and water temperature of the spawning grounds,[22)] it cannot be said that genetic ramification among populations has necessarily (439) been corroborated, and it is thought it would be proper to await future genetic research such as by electrophoresis to draw conclusions. The only thing is that, whichever the case may be, the fact that a population structure that ought to be called a breed sphere as proposed in the preceding report[1)] was confirmed morphologically as well is thought to be worthy of attention.

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